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ERRATUM

Survival Chances of Mutants Starting With One Individual

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Abstract A simple theoretical model of a Darwinian system (a periodic system with a multiplication phase and a selection phase) of entities (initial form of polymer strand, primary mutant and satellite mutants) is given. First case: one mutant is considered. One individual of the mutant appears in the multiplication phase of the first generation. The probabilities to find N individuals of the mutant $W_{\mathrm{n}}^{\mathrm{S}}(N)$ after the multiplication phase M of the n-th generation (with probability δ of an error in the replication, where all possible errors are fatal errors) and $W_{\mathrm{n}}^{\mathrm{S}}(N)$ after the following selection phase S (with probability β that one individual survives) are given iteratively. The evolutionary tree is evaluated. Averages from the distributions and the probability of extinction $W_{\infty}^{\mathrm{S}}(0)$ are obtained. Second case: two mutants are considered (primary mutant and new form). One individual of the primary mutant appears in the multiplication phase of the first generation. The probabilities to find N_{p} individuals of the primary mutant and N_{m} individuals of the new form $W_{\mathrm{n}}^{\mathrm{M}}\left(N_{\mathrm{p}},\ N_{\mathrm{m}}\right)$ after the multiplication phase M of the n-th generation (probability ε of an error in the replication of the primary mutant giving the new form) and $W_{\mathrm{n}}^{\mathrm{S}}\left(N_{\mathrm{p}},\ N_{\mathrm{m}}\right)$ after the following selection phase S (probabilities β_{p} and β_{m} that one individual each of the primary mutant and of the new form survives) are given iteratively. Again the evolutionary tree is evaluated. Averages from the distributions are obtained.

Keywords Darwinian system · Multiplication · Error in replication · Selection · Initial form · Primary mutant · Satellite mutants · Bernoulli polynomial · Probability distribution · Evolutionary tree · Complementary and anti-parallel replication · Plus-strand · Minus-strand · Translation apparatus · Origin of life

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Owing to an error in the production process, the following article has been published incorrectly online. The article including the illustrations is presented hereafter.

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1 Introduction: Darwinian System

1.1 Average Number of Individuals of the Mutant

In a simple theoretical model of a Darwinian system proposed by the present author and others [1–4], there is a multiplication phase M and selection phase S (Fig. 1) of a population of entities (e.g. polymer strands of different folding structures due to different sequences). In the multiplication phase the strands replicate by multiplication factor ρ (with the number s of subsequent replication steps, $\rho = 2^s$). In the selection phase, a single strand survives with probability β. The multiplication factor per generation is $r = \rho\beta$.

For the initial form let us suppose $r = 1$, then then the total population stays constant. One individual of the primary mutant appears with $r > 1$, where the surviving probability β for the primary mutant is larger than for the initial form. Thus the average number of the primary mutants is $Z_n = r^n$ after n generations if supply is not the limiting factor. There must be a cut-off when the limit of supply is reached (Fig. 2).

1.2 Primary Mutant and Satellite Mutants

Consider the average number Z of a primary (error-free) individuals of the mutant and Z_{kF} of satellite (k-errors containing) mutants (Fig. 3). This state is reached from one generation to the next by replication either with one additional error in a copy of a $(k-1)$-error containing mutant (factor $(\rho-1)\ \eta$ in first approximation, diagonal paths in Fig. 3) or with no additional error in a copy of a k-error containing mutant (factor $\rho-(\rho-1)\ \eta$ in first approximation, horizontal paths in Fig. 3). The probability that an error occurs in a given strand is given by η. Selection of mutants occurs with probability $\beta > \beta_{1F} > \beta_{2F} > \ldots, > \beta_{kF}$. Considering the steady state, the values Z, Z_{1F}, Z_{2F}, ... Z_{kF} from one generation (left side in Fig. 3) to the next generation (right side in Fig. 3) are identified; note that $[\rho - (\rho - 1)\eta]\beta = 1$ and $\alpha_k = (\rho - 1)\,\eta\,\beta_{kF}/[1 - (\rho - (\rho - 1)\,\eta)\,\beta_{kF}]$. Assuming $\alpha_k = \alpha/k$ for simplicity, then $Z_{kF} = (\alpha/k)\ Z_{(k-1)F} = (\alpha_k/k!)Z$, and with $Z_{total} = Z + Z_{1F} + Z_{2F} + \ldots = Ze^{\alpha}$ we find

$$Z_{kF}/Z_{total} = (\alpha_k/k!)/e^{\alpha} \tag{1}$$

and this result is shown graphically in Fig. 4.

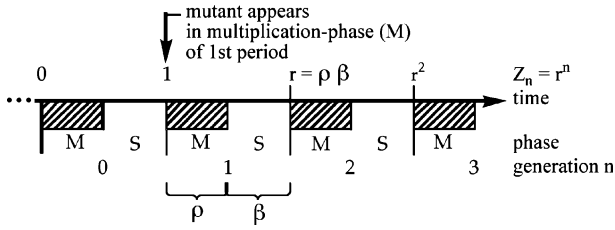

Fig. 1 Darwinian system with a multiplication phase M and a selection phase S of an entity (polymer strand). One mutant appears at the beginning of first generation. The average number of individuals of the mutant after n generations, if supply is not the limiting factor, is Z_n. The multiplication factor is ρ, and β is the probability that an individual of the mutant survives during selection phase

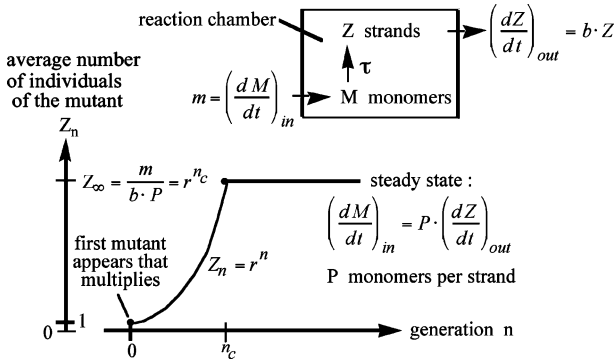

Fig. 2 Cut-off Z_∞ of the average number of individuals of the mutant, when the limit of supply is reached (steady state in reaction chamber)

2 Probability Distribution of N Individuals of the Mutants

2.1 One Mutant Considered

The probability to find N ($\leq N_{\max}$) individuals of the mutant after the selection phase S (dots (•) in the evolutionary trees in Figs. 6 and 7) of the n-th generation is given by the Bernoulli polynomial (Fig. 5a)

$$W_{\mathrm{n}}^{\mathrm{S}}(N) = \sum_{\nu=N}^{N_{\max}} W_{\mathrm{n}}^{\mathrm{M}}(\nu) \bullet \binom{\nu}{N} (1-\beta)^{(\nu-N)} \beta^{\mathrm{N}} \tag{2}$$

where β is the probability that one individual of the mutant survives.

The probability to find N ($\leq N_{\max}$) number of mutants after the multiplication phase M (circles (○) in the evolutionary trees in Figs. 6 and 7) of the $(n+1)$-th generation is given by the Bernoulli polynomial (Fig. 5b)

$$W_{\mathrm{n+1}}^{\mathrm{M}}(N) = \sum_{\nu=L(N)}^{N} W_{\mathrm{n}}^{\mathrm{S}}(\nu) \bullet \binom{\mu-\nu}{N-\nu} \delta^{(\mu-N)} (1-\delta)^{(N-\nu)} \tag{3}$$

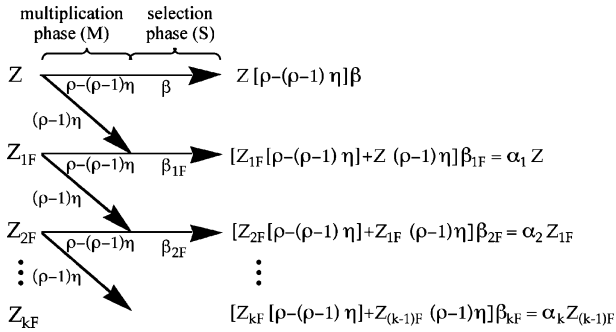

Fig. 3 Average number Z of a primary (error-free) mutant and Z_{kF} of satellite (k-errors containing) mutants. Diagonal paths: one additional error in a copy of a $(k-1)$-error containing mutant. Horizontal paths: no additional error in a copy of k-error containing mutant. Probability η that an error occurs in a given strand. Selection of mutants occurs with probability $\beta > \beta_{1F} > \beta_{2F} > \ldots, > \beta_{kF}$. Steady state for values Z, Z_{1F}, Z_{2F}, ... Z_{kF}

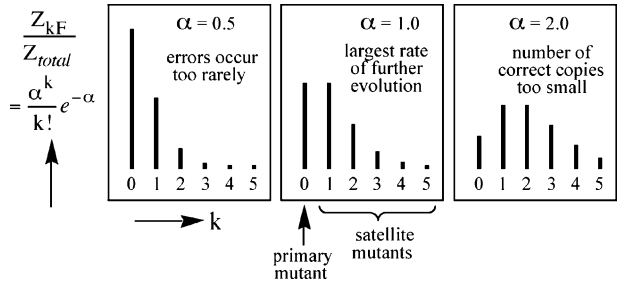

Fig. 4 Primary (error-free) mutant and satellite (k-error containing) mutants. The corresponding average numbers are Z and Z_{kF}

where δ is the probability that a copy of the mutant has a fatal error, where all possible errors are fatal errors, $\mu = \begin{cases} 2\nu & 2\nu \le N_{max} \\ N_{max} & 2\nu > N_{max} \end{cases}$ the cut-off condition when the limit of supply is reached and $L(N) = \begin{cases} N/2 \; even & N \\ (N+1)/2 \; odd & N \end{cases}$.

The evolution trees (Figs. 6 and 7) are given by the initial probability $W_{initial}(1) = 1$ that one individual of the mutant appears: $W_1^M(1) = W_{initial}(1)\delta = \delta$ and $W_1^M(2) = W_{initial}(1)(1-\delta) = (1-\delta)$.

The numerical evaluations are given in Figs. 8, 9, and 10. The average number Z_n of the mutant is evaluated from the probability distribution (Figs. 8 and 9) for the r^n-regime (n=9) and for the Z_∞−regime $(n = 30)$. The probability of extinction $W_\infty^S(0)$ as function of δ and β is given in Fig. 10. With three subsequent replication steps in each multiplication phase (Fig. 10b) the multiplication factor ρ=8 and smaller β values become accessible.

2.2 Two Mutants Considered

The probability to find N_p individuals of the primary mutant and N_m number of the new form $\left(N_p + N_m = N \le N_{max}\right)$ after the selection phase S of the n-th generation is given by the Bernoulli polynomial (Fig. 11a)

$$W_n^S(N_p,\, N_m) = \sum_{\nu_p=N_p}^{q} \sum_{\nu_m=N_m}^{q} W_n^M(\nu_p,\, \nu_m) \cdot \binom{\nu_p}{N_p} \left(1-\beta_p\right)^{(\nu_p - N_p)} \beta_p^{N_p} \cdot \binom{\nu_m}{N_m} (1-\beta_m)^{(\nu_m - N_m)} \beta_m^{N_m} \tag{4}$$

where β_p (β_m) is the probability that one individual of the primary mutant (of the new form) survives.

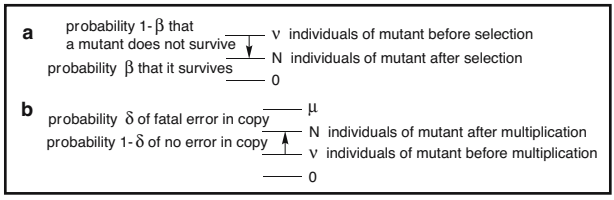

Fig. 5 Sketch of how Bernoulli polynomial is applied, case of the probability distribution of a single mutant. (**a**) Selection phase, Equation (2). (**b**) Multiplication phase, Equation (3). (μ-ν) total copies of mutant, (N-ν) error-free copies of mutant. All possible errors are fatal errors

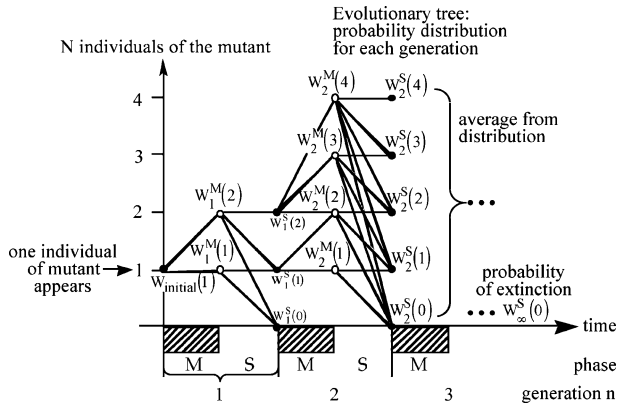

Fig. 6 Evolutionary tree of the mutant. Probability distributions (Equations (3 and (2)) of finding N individuals of the mutant after the multiplication phase (○) and after the selection phase (•) for each generation starting with one individual of the mutant. The probability of extinction is $W_{\infty}^{S}(0)$

The probability to find N_p individuals of the primary mutant and N_m individuals of the new form $\left(N_p + N_m = N \leq N_{max}\right)$ after the multiplication phase M of the (n+1)-th generation is given by the Bernoulli polynomial (Fig. 11b)

$$W_{n+1}^{M}\left(N_p, N_m\right) \sum_{\nu_p=0}^{\nu} \sum_{\nu_m=0}^{\nu-\nu_p} \sum_{g_p=0}^{\mu_p-\nu_p} = W_n^{S}\left(\nu_p, \nu_m\right) \cdot \begin{pmatrix} \mu_p - \nu_p \\ g_p \end{pmatrix} \varepsilon^{g_p} (1-\varepsilon)^{\left(\mu_p - g_p - \nu_p\right)} \quad (5)$$

where ε is the probability that an error in copying the primary mutant occurs and the new form emerges and, $\mu_p = \begin{cases} 2\nu_p & 2\nu \leq N_{max} \\ (\nu_p/\nu)N_{max} & 2\nu > N_{max} \end{cases}$ and $\mu_m = \begin{cases} 2\nu_m & 2\nu \leq N_{max} \\ (\nu_m/\nu)N_{max} & 2\nu > N_{max} \end{cases}$ are the cut-off conditions when the limit of supply is reached.

The evolutionary tree is given by the initial probability $W_{initial}\left(N_p = 1,\ N_m = 0\right) = 1$ that one individual of the primary mutant appears: $W_1^{M}\left(N_p = 2, N_m = 0\right) = (1-\varepsilon)\ W_{initial}(1,\ 0) = 1-\varepsilon$ and $W_1^{M}\left(N_p = 1, N_m = 1\right) = \varepsilon W_{initial}(1, 0) = \varepsilon$. The formalism can be applied to systems with time-dependent ε (changing exposition to mutagene): in Fig. 12a ε is assumed to be time-independent, in Figs. 12b, c and 13 ε is chosen to have a smooth peak at $n = 50 \pm 5$.

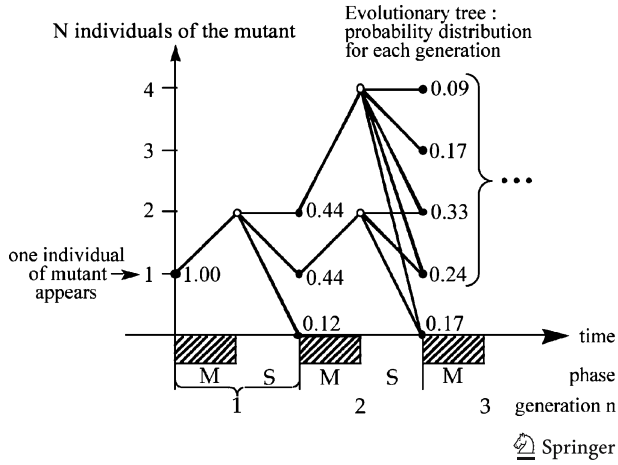

Fig. 7 Evolutionary tree for the simple case where: δ=0 (no errors occurring), β=2/3 and ρ=2 (one replication step in multiplication phase)

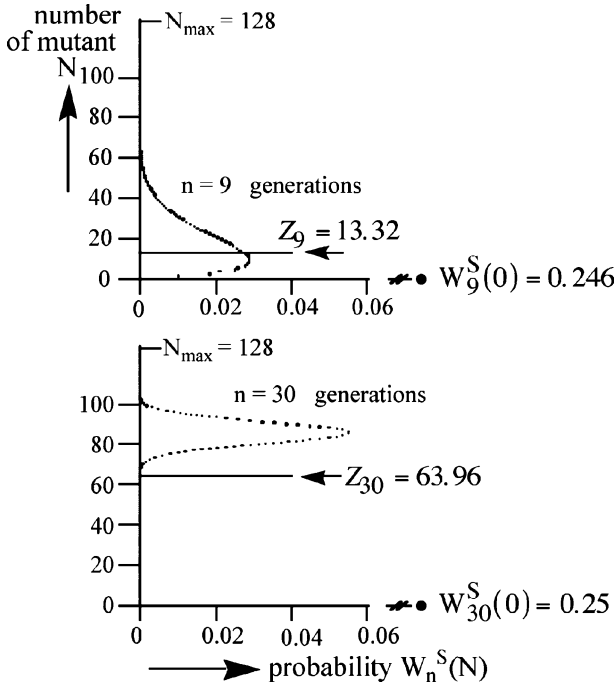

Fig. 8 Probability distributions (continued from Fig. 7) of finding N individuals of the mutant after the selection phase at generations n=9 and n=30. We assume a limited monomer supply ($N_{max}=2^7=128$)

2.3 Elimination of the (−)-*R*-Strand, Retention of the (+)-*R*-strand: A Crucial Step in Origin of Life

Starting from a "RNA-world" (*R*-strands building Hairpin-Assembler devices) and introducing A-monomers (which interlink to the HA-devices such that they become bound and form an A-oligomer) it is shown that a simple translation apparatus evolves (HAE-device producing enzymes [1–4]). In this "RNA-protein world" the complementary and anti-parallel copy of the (+)-assembler (carrying the recipe to produce an enzyme) is a (−)-assembler (its HAE-device producing nonsensical agglutinate).

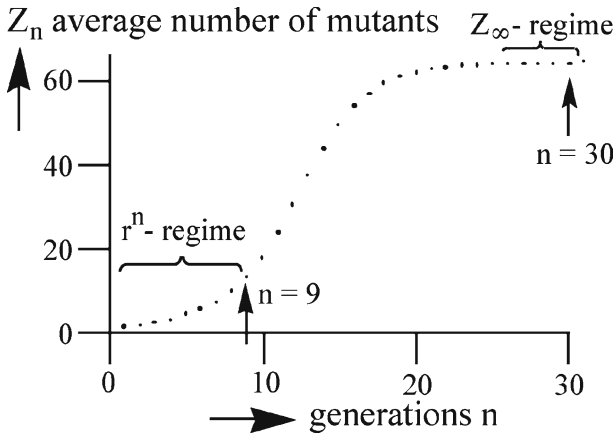

Fig. 9 Average number Z_n of individuals of the mutant evaluated from probability distribution (note that the probability of extinction $W_\infty^s(0)$ must be taken into account). The two cardinal examples (Fig. 8) n=9 (r^n-regime: $r=\rho\beta=4/3$, $(4/3)^9=13.32$) and n=30 (Z_∞ – regime : Z_∞ = 64.0) are indicated by arrows

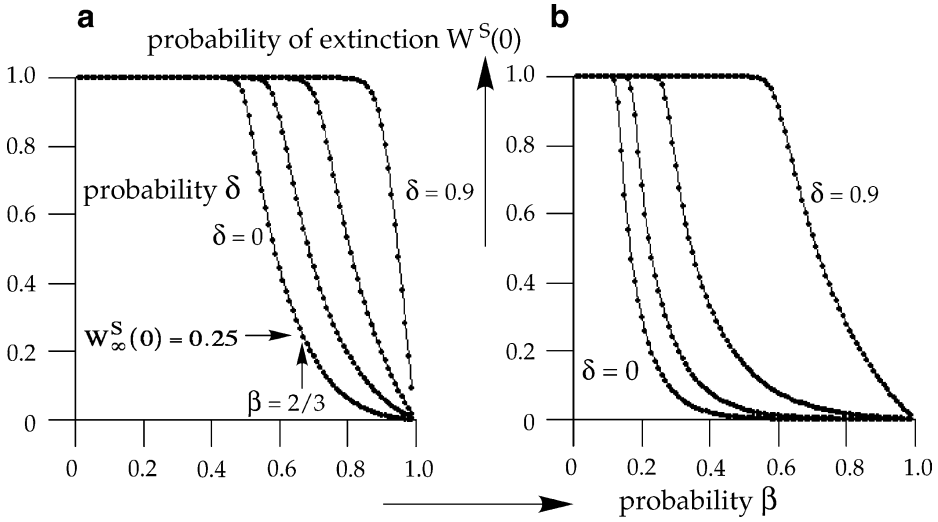

Fig. 10 Probability of extinction $W^s_\infty(0)$ as a function of δ and β. (**a**) One subsequent replication step in each multiplication phase (ρ=2). The case of Figs. 7, 8, 9 (δ=0 and β=2/3, $W^s_\infty(0) = 0.25$) are indicated by arrows. (**b**) Three subsequent replication steps in each multiplication phase (ρ=8)

Later on D-strands are introduced, which are not capable of participating in the synthesis of A-oligomers. In the "DNA-RNA-protein world" the mixture of (+)-assembler and (−)-assembler is unstable eliminating (−)-assembler: (+)-*R*-strands having (−)-*D*-strands as template and (−)-*D*-strands having (+)-*R*-strands as template will be selected. These (−)-*D*-strands become carriers of the genetic information.

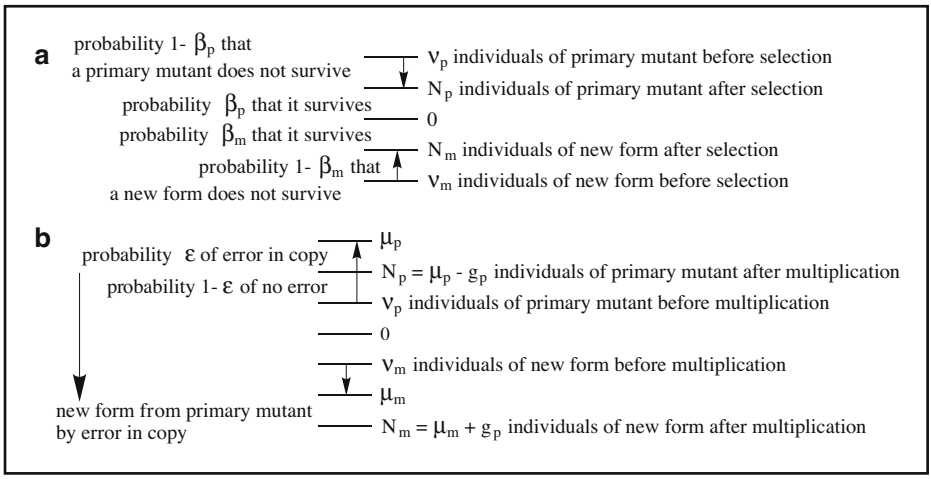

Fig. 11 Sketch of how Bernoulli polynomial is applied, case of the probability distribution of two mutants. (**a**) Selection phase, Equation (4). (**b**) Multiplication phase, Equation (5). There are (μ_p-ν_p) total copies of the primary mutant, (N_p–ν_p) error-free copies of the mutant, (μ_m–ν_m) total copies of the new form, (μ_p–N_p) error-containing copies of the primary mutant which give the new form

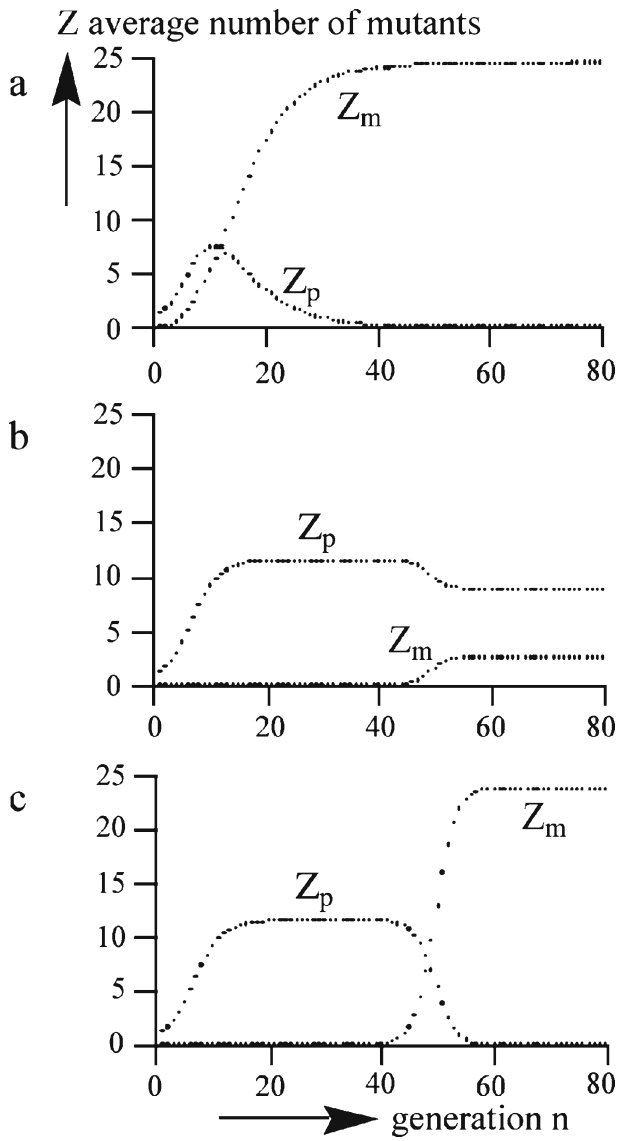

Fig. 12 Average number of individuals of the primary mutant and the new form Z_p and Z_m evaluated from the probability distribution. There are two subsequent replication steps in each multiplication phase ($\rho = 4$), and we assume limited monomer supply ($N_{max} = 2^6 = 64$). (**a**) Probability of error resulting in new form ($\varepsilon = 0.005$), probability that primary mutant and new form survives ($\beta_p = 0.33$ and $\beta_m = 0.67$). (**b**) and (**c**) $\varepsilon = 0.05$ sech [(n-50)/2] (smooth peak at $n = 50 \pm 5$), $\beta_p = 0.33$. (**b**) $\beta_m = 0.33$. (**c**) $\beta_m = 0.67$

This elimination of the (−)-assembler is treated simply as in the following (the numerical evaluation is given in Fig. 15). For the selection phase we use Equation (4) with the probability $\beta_p > \beta_m$ that a (+)-*R*-strand or a (−)-*R*-strand survives, respectively (Fig. 11a). For the multiplication phase in the "RNA-protein world" we use the replication rule (Fig. 14a):

$$\begin{aligned} N_p &= \nu_p + \nu_m \\ N_m &= \nu_p + \nu_p. \end{aligned} \tag{6}$$

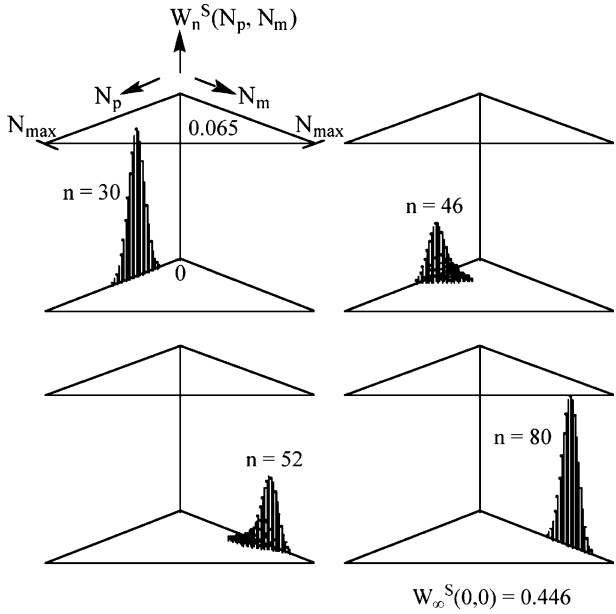

Fig. 13 Probability distribution $W_n^S(N_p, N_m)$ of finding N_p individuals of the primary mutant and N_m individuals of the new form ($N_p + N_m = N \leq N_{max} = 64$) after the selection phase (cases from Fig. 12c) in the *n*-th generation (indicated)

In the "DNA-RNA-protein world" we use the replication rule (Fig. 14b):

$$\begin{aligned} N_p &= 2\nu_p \\ N_m &= 2\nu_m. \end{aligned} \tag{7}$$

3 Conclusion

A simple theoretical model of a Darwinian system is given. Probability distributions for replication and for selection (Bernoulli polynomials) are applied iteratively. The cases of only one mutant and of two mutants (primary mutant and new form) are considered. The formalism is applied to a crucial step in the origin of life: the elimination of the (−)-*R*-strand and retention of the (+)-*R*-strand.

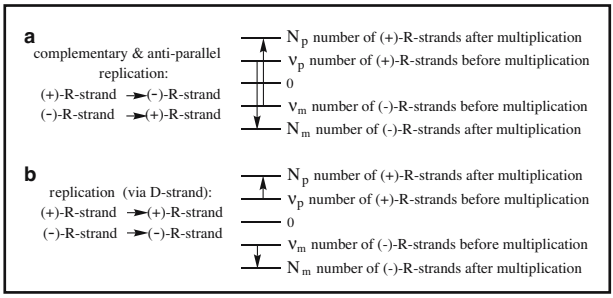

Fig. 14 Multiplication phase. Sketch of replication rule in the (**a**) "RNA-protein world" given by Equation (6), (**b**) "DNA-RNA-protein world" given by Equation (7)

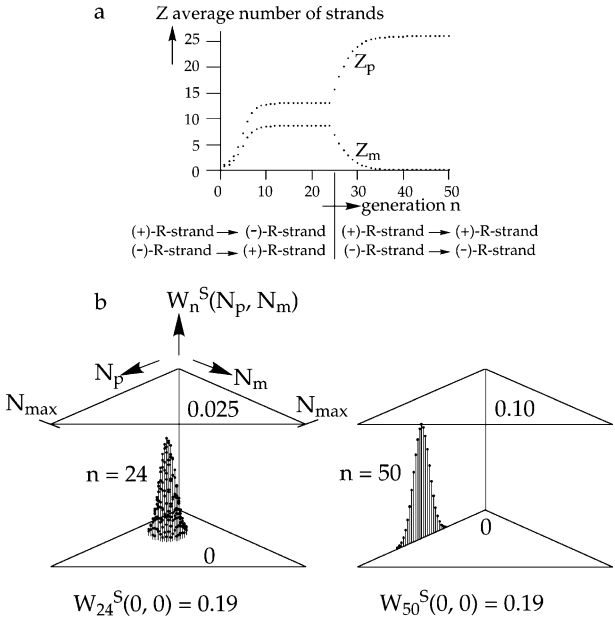

Fig. 15 (**a**) Average number Z_p and Z_m of strands evaluated from the probability distribution, (**b**) probability distribution $W_n^S(N_p, N_m)$ of finding N_p number of (+)-R-strand and N_m number of (-)-R-strand after the selection phase in the *n*-th generation (indicated) before and after the transition. Transition at generation $n = 25$. Probability that (+)-R-strand and (-)-R-strand survives are (β_p=0.33 and β_m=0.50), two subsequent replication steps in each multiplication phase (ρ=4), limited monomer supply ($N_{max} = 64$)

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